comprising genome of 2504 unselected individuals collected worldwide. The combination of 184 SNPs associated with PTC was used to group individuals in different risk-clusters according to their genetic structure, calculated by Bayesian statistics, as previously performed for polycystic ovary syndrome [2]. Individuals were distributed among 7 groups worldwide, indicating different degree of genetic predisposition to PTC. We then considered genetic data from about 1200 individuals (697 PTC *versus* 497 healthy controls) of Central/South Italian origin registered in a GWAS, specific for PTC [3]. This first analysis was refined using the 33 SNPs reasonably most causative of genetic clustering (26 with $p<0.05$ at trend test in GWAS and 7 with $p<0.05$ in the model of recessive inheritance). At multivariate logistic regression analysis, PTC and healthy controls resulted genetically different (ODDS RATIO 188.6, 95%CI 64.35-552.8), revealing diverse predisposition to develop cancer. Afterwards, these results have been confirmed in an independent cohort of Italian subjects (234 PTC and 100 controls). Then, the genetic structure of each subject was indicated as a percentage of affinity to each risk-cluster and re-analyzed together with other risk factors: sex, body-mass index, area of origin and familiarity (quantified in a growing score as the degree of kinship increases). These data were analyzed together by principal component analysis and clustering of the two groups was even more pronounced. The most contributive factors to the diversity between PTC and healthy controls were genetics and familiarity.

CONCLUSION. We demonstrated that PTC affected subjects are genetically different from healthy controls, and that the difference is identifiable in a peculiar combination of genetic variants.

REFERENCES

1. Bray F et al. CA: a cancer journal for clinicians. 2018; 68 (6):394-424

2. Casarini and Brigante. JCEM. 2014; 99:E2412-20

3. Köhler et al. Genome-wide association study on differentiated thyroid cancer. J Clin Endocrinol Metab. 2013;98:E1674-81.

Neuroendocrinology and Pituitary

PITUITARY TUMORS II

AIP Gene Germline Mutations in Non-Selected Patients with Apparently Sporadic Pituitary Macrodenomas

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MON-300

Up to 5% of all pituitary tumors are hereditary (e.g. due to menin or AIP genes germline mutations). AIP gene mutations are more common in subjects with acromegaly, less than 30 years old at the onset of disease, and with FIPA family history.

The study was aimed at the assessment of the frequency and characteristics of AIP-mutation related tumors in non-selected patients with pituitary macroadenomas.

Material and methods. The study included subsequent 131 patients (57 males, 74 females; median age 42 years (IQR 25 years) diagnosed with pituitary macroadenomas, and with a negative family history of FIPA or MEN1 syndromes. The following tumors were identified: 11 ACTH-secreting, 49 GH-secreting (including 7 pluri-hormonal ones), 6 gonadotropinomas, 23 prolactinomas, 1 TSH-oma, and 43 non-secreting adenomas. Sanger sequencing was used for the assessment of AIP gene variants. The study was approved by the Ethics Board of JUMC.

Results. An AIP mutation was identified in five of 131 included subjects (3.8%): one diagnosed with Cushing's disease, two with acromegaly, and two with non-secreting adenomas. In two patients, the identified mutation usually predisposes to ACTH-secreting adenomas, in two patients - mutations of unknown clinical significance were found (usually connected with pituitary adenomas), and the mutation detected in one patient was described as benign. Patients harboring hereditary AIP gene variations did not differ from the rest of the study group in median age at diagnosis (41 vs. 42.5 years, p=0.8), median largest tumor diameter (25 vs. 24 mm, p=0.6), gender distribution (60% of females vs. 56.3%, p=0.8), secreting tumor frequency (60% vs. 67.5%, p=0.7), or acromegaly diagnosis frequency (40% vs.37.3%, p=0.9). 2 of the 5 patients with identified AIP gene mutations agreed for their families to be offered AIP genetic testing: (1) An AIP mutation was found in the asymptomatic mother of one acromegalic female patient. (2) The AIP mutation of unknown clinical significance was detected in the son of a male acromegalic patient with acromegaly, clinically unscreened yet.

Conclusions. In our series of apparently sporadic pituitary macroadenomas, AIP gene mutation carriers did not differ substantially from patients with negative genetic testing. A risk factor-centered approach to AIP genetic screening may result in missing germline mutations, therefore, there is a need to establish if such a situation negatively impacts a patient's and his/her family outcomes.

Diabetes Mellitus and Glucose Metabolism

CLINICAL AND TRANSLATIONAL GLUCOSE METABOLISM AND DIABETES

Frequency and Associated Factors with Multidrug-Resistant Organism Infection in Diabetic Foot Ulcers in a Peruvian Public Hospital

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MON-626

Objective: To determine the frequency and associated factors with multidrug-resistant organism (MDRO) infection among patients with diabetic foot ulcers in a Peruvian Public Hospital.

Materials and methods. Cross-sectional survey was conducted from January 2017 -December 2018 at National

Hospital in Lima Perú. Ulcers with clinical signs of infection (erythema, edema, pain, purulent exudate) according Infectious Diseases Society of America clinical practice guideline were included[1]. Wounds with only skin involvement were excluded. On admission, specimens for culture were obtained after cleansing and debriding of the wound. Samples were promptly sent to the microbiology laboratory for culture using appropriate transport media. Bacterial identification and antibiotic susceptibility testing were performed using the VITEK® 2 automated system (BioMérieux Laboratory, Argentina). Multidrug-resistant organisms were identified according to the recommendations of International Expert Proposal[2]. Prevalence ratios derived from bivariate analysis are given with their 95% CI, which was performed to study factors associated with the presence of multidrug-resistant bacteria; and a multivariate analysis with a lineal model to associated variables found in the bivariate analysis. This study has the approval of the Research Ethics Committee of the María Auxiliadora Hospital.

Results Among 153 selected subjects, 75% were male, with an average age of 59 yo, 70% had ≥10 years of diabetes duration and only 16% had HbA1C <7%. A frequency of 85% of patients with MDRO infection was found and was associated with minor amputation RP 1.18 (95% CI 1.01-1.44) and with hospitalization time of ≥ 28 days RP 1.21 (95% CI 1.03-1.30).

Conclusion. 6 of 7 patients have MDRO infection among patients with diabetic foot ulcers and are associated with the occurrence of minor amputation and hospitalization time ≥ 28 days.

References

1. Lipsky BA, *et al*. 2012 Infectious Diseases Society of America clinical practice guideline for the diagnosis and treatment of diabetic foot infections. Clin Infect Dis. 2012;54(12):e132-73.

2. Magiorakos AP, *et al*. Multidrug-resistant, extensively drug-resistant and pandrugresistant bacteria: an international expert proposal for interim standard definitions for acquired resistance. Clin Microbiol Infect. 2012;18(3):268-81.

Neuroendocrinology and Pituitary

CASE REPORTS IN SECRETORY PITUITARY PATHOLOGIES, THEIR TREATMENTS AND OUTCOMES

An Asynchronous Double Growth Hormone Secreting Pituitary Adenoma as a Cause of Rapid Tumor Regrowth After Initially Successful Surgery

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SAT-265

Background. Double pituitary adenomas are a rare entity, which requires clinical attention and a careful follow-up. Case report. A 37-year-old man presented with left-sided painful gynecomastia. He denied typical symptoms of excessive growth hormone (GH) secretion and did not show any acromegalic features. Due to low testosterone and LH levels with mild hyperprolactinaemia, the patient was referred to pituitary MR, which revealed an 11x13 mm right-sided sellar tumor. An increased IGF-1 was noted subsequently (1482 ng/mL; N 109-284 ng/mL), together with the lack of GH suppression in OGTT. Transphenoidal resection of pituitary tumor performed in 2012 led to biochemical (IGF-1 260 ng/mL, GH 0.08 ng/mL) and radiological remission of the disease. A histopathology report revealed a densely granulated somatotropic pituitary adenoma with mild nuclear atypia, expressing somatostatin receptors [sstr2A (+), sstr5 (+/-)]. Due to gradually increasing IGF-1 levels (with low, although rising, GH values ranging from 0.07 to 0.92 ng/mL) in subsequent years, OGTT was repeated in 2015, showing appropriate GH suppression. In 2016, however, acromegaly recurrence was confirmed both biochemically (increasingly high IGF-1 - 664 ng/mL - and unsuppressed post-OGTT growth hormone) and in MR imaging. The patient was reoperated in June 2017. The second histopathology reported an oncocytic somatotropic acidophil stem cell pituitary adenoma with Ki-67 >3% and mitotic figures. Subsequent anterior pituitary lobe insufficiency (adrenal, thyroid and gonadal axis) was found and adequately treated. Complete tumor removal was confirmed by MR performed three months after repeated surgery, as well as a low GH level (0.97 ng/mL), although accompanied by borderline IGF-1 values (277 ng/mL). Eighteen months after surgery, the recurrence of acromegaly was again confirmed, with adenoma regrowth and increased GH (2.31 ng/mL) and IGF-1 (474 ng/mL) levels. Octreotide LAR was started (despite retina wrinkling which was observed when lanreotide was administered before the first surgery), which led to a normalization of GH (0.96 ng/mL) and IGF-1 levels (152 ng/mL), as well as partial pituitary tumor regression after six months therapy. Conclusion. In a case of GH-secreting pituitary adenoma recurrence after apparent successful surgery, a double pituitary tumor with more aggressive histology should be considered.

Diabetes Mellitus and Glucose Metabolism

CLINICAL AND TRANSLATIONAL GLUCOSE METABOLISM AND DIABETES

Quality of Life in a Pragmatic Trial of a Type 1 Diabetes Adolescent Transition Program

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MON-631

Introduction: Adolescents with type 1 diabetes (T1D) experience ongoing deterioration in their glycemic control as they transition to young adulthood.[1] Several trials have evaluated possible transition interventions to ameliorate the care gap between pediatric and adult services in